Type: Poster Presentation

Final Abstract Number: 41.064
Session: Poster Session I
Date: Thursday, March 3, 2016
Time: 12:45-14:15
Room: Hall 3 (Posters & Exhibition)

Detection of carbapenemase genes OXA-48, VIM, IMP, KPC and NDM in carbapenemase-producing klebsiella pneumoniae isolates from blood cultures of hospitalized patients in Istanbul, Turkey

F. Koksal Cakirlar[1,*], N. Gonullu[1], F. Kalayci[2], N. Kiraz[1]

[1] *Istanbul University Cerrahpasa Faculty of Medicine, Istanbul, Turkey*
[2] *Istanbul Yeni Yuzyıl University Medical Faculty, Istanbul, Turkey*

Background: Carbapenemase-producing *Klebsiella pneumoniae* (CPK) isolates have emerged as major causes of health care-associated infections worldwide. The present study was conducted to investigate the most prevalent carbapenemase genes; *bla*OXA-48, *bla*VIM, *bla*IMP, *bla*NDM and *bla*KPC in CPK isolates from blood culture of hospitalized patients at Istanbul University Cerrahpasa Medical School hospital.

Methods & Materials: Between January 2012 and October 2015, a total of 100 CPK isolates were isolated from blood culture samples of hospitalized patients with bacteremia in intensive care units and in various departments of our hospital. Blood cultures were analyzed with the BACTEC system (Becton Dickinson,USA). The identification and antimicrobial resistance of CPK isolates were determined by Phoenix automated system (BD Diagnostic Systems, Sparks, MD). The detection of carbapenemase genes was performed by real-time PCR using MDR KPC/OXA Real-TM and MDR MBL (VIM, IMP, NDM) Real-TM PCR kit (Sacace Biotechnologie, Italie).

Results: ESBL rate was 87% in CPK isolates. All isolates were phenotypically positive for carbapenemase activity. The isolates were highly resistant to cefuroxime (96%), and amoxicillin/clavulanic acid (91%), ceftriaxone, cefotaxime, ceftazidime (87%), piperacillin/tazobactam (86%), cefepime (82%), ciprofloxacin (76%) and gentamicin (65%). Amikacin resistance rate was 18%. Colistin and tigecycline resistance rates were 1%. The carbapenemase gene *bla*OXA-48 was detected in 43% of isolates and *bla*VIM in 5%. One isolate harbored a combination of *bla*OXA-48 and *bla*VIM. None of the isolates harbored *bla*NDM, *bla*KPC or *bla*IMP.

Conclusion: The carbapenemase genes *bla*OXA-48 with *bla*VIM was isolated in one of our isolates. Significant effort must be made to prevent the spread of CPK and continuous monitoring of drug resistance is necessary in our clinical settings.

http://dx.doi.org/10.1016/j.ijid.2016.02.259

Type: Poster Presentation

Final Abstract Number: 41.065
Session: Poster Session I
Date: Thursday, March 3, 2016
Time: 12:45-14:15
Room: Hall 3 (Posters & Exhibition)

Detection of IMP, VIM and NDM metallo-betalactamase carbapenemase genes in carbapenem resistant pseudomonas strains from bloodstream infections in Istanbul, Turkey

F. Yilmaz Yucel, F. Koksal Cakirlar*, E. Koyuncu, R. Ozturk

Istanbul University, Cerrahpasa Faculty of Medicine, Istanbul, Turkey

Background: Carbapenem–resistant *Pseudomonas aeruginosa* causing various life-threatening infections is an important problem worldwide. Carbapenemase genes are one of the most common mechanisms reported in carbapenem-resistant *P. aeruginosa*. In this study, we aimed to determine the presence of IMP, VIM and NDM metallo-betalactamase (MBL) carbapenemase genes.

Methods & Materials: Between 2011 and 2015, a total of 48 carbapenem–resistant/intermediate *Pseudomonas* strains were isolated from blood samples of patients with bacteremia who were hospitalized in intensive care units and in various departments at Istanbul University Cerrahpasa Medical Faculty hospital. Blood cultures were analyzed with the BACTEC system (Becton Dickinson, USA). The identification and antimicrobial resistance of the strains were determined by Phoenix automated system (BD Diagnostic Systems, Sparks, MD). Phenotypic MBL E-test was used to investigate the presence of MBL enzymes. All study strains were screened by multiplex PCR for the presence of MBL genes.

Results: The species distribution was as follows: *P. aeruginosa* 42 (87.5%), *P. putida* 5 (10,4%) and *P. fluorescens* 1(2.1%). Thirty six (76%) of isolates were carbapenem-resistant (MIC 8-≥32 μg/mL), 12 (25%) intermediate resistant (MIC 6 μg/mL). MIC50 and MIC90 were respectively 32 μg/mL and 32 μg/mL to both imipenem and meropenem. Resistance rates of the isolates to the antibacterial agents, respectively, were as follows: sefepim and ticarcillin 56%, levofloxacin 52%, ciprofloxacin 50%, ceftazidime 48%, piperacillin/tazobactam 46%, tobramycin and netilmycin 44%, gentamicin and aztreonam 37.5%, and amikacin 29%. None of the isolates were resistant to colistin. MBL screening with EDTA was positive in 6.3% (n = 3). In these three isolates with MBL positive, VIM type MBL gene was detected in two *P. aeruginosa* and one *P. putida*. NDM and IPM-type MBL genes were not in any of the isolates.

Conclusion: In our study, VIM type MBL gene was first shown in *Pseudomonas* strains at our hospital. Therefore, identification of carbapenemase genes restricting treatment options is important to rational antibiotic use and also to implement infection prevention measures to reduce their spreading.

http://dx.doi.org/10.1016/j.ijid.2016.02.260